

```

1  GTGACTGCTATCACCTTGGCGGTCTCTTGTTGAAAGGAATAATTACTCTAGTGTCTGACT
   -----+-----+-----+-----+-----+-----+ 60
   M T A I T L G G L L L K G I I T L V S T
61  CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC
   -----+-----+-----+-----+-----+-----+ 120
   H T S S T L P A F K K I L V A N R G E I
121 GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC
   -----+-----+-----+-----+-----+-----+ 180
   A V R A F R A A L E T G A A T V A I Y P
181 CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACT
   -----+-----+-----+-----+-----+-----+ 240
   R E D R G S F H R S F A S E A V R I G T
241 GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA
   -----+-----+-----+-----+-----+-----+ 300
   E G S P V K A Y L D I D E I I G A A K K
301 GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCTGTCTGAAAATGCCCAGCTTGCC
   -----+-----+-----+-----+-----+-----+ 360
   V K A D A I Y P G Y G F L S E N A Q L A
361 CGCGAGTGC GCGGAAAACGGCATTACTTTTATTGGCCCAACCCAGAGGTTCTTGATCTC
   -----+-----+-----+-----+-----+-----+ 420
   R E C A E N G I T F I G P T P E V L D L
421 ACCGGTGATAAGTCTCGTGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTGGCG
   -----+-----+-----+-----+-----+-----+ 480
   T G D K S R A V T A A K K A G L P V L A
481 GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC
   -----+-----+-----+-----+-----+-----+ 540
   E S T P S K N I D D I V K S A E G Q T Y
541 CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA
   -----+-----+-----+-----+-----+-----+ 600
   P I F V K A V A G G G G R G M R F V S S
601 CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCCGGC
   -----+-----+-----+-----+-----+-----+ 660
   P D E L R K L A T E A S R E A E A A F G
661 GACGGTTCGGTATATGTGCAACGTGCTGTGATTAACCCCCAGCACATTGAAGTGCAGATC
   -----+-----+-----+-----+-----+-----+ 720
   D G S V Y V E R A V I N P Q H I E V Q I

```

FIG. 1A

```

CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT
721 -----+-----+-----+-----+-----+-----+ 780
      L G D R T G E V V H L Y E R D C S L Q R
CGTCACCAAAAAGTTGTGCGAAATTGCGCCAGCACAGCATTGGATCCAGAACTGCGTGAT
781 -----+-----+-----+-----+-----+-----+ 840
      R H Q K V V E I A P A Q H L D P E L R D
CGCATTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC
841 -----+-----+-----+-----+-----+-----+ 900
      R I C A D A V K F C R S I G Y Q G A G T
GTGGAATTCCTGGTCGATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC
901 -----+-----+-----+-----+-----+-----+ 960
      V E F L V D E K G N H V F I E M N P R I
CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG
961 -----+-----+-----+-----+-----+-----+ 1020
      Q V E H T V T E E V T E V D L V K A Q M
CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC
1021 -----+-----+-----+-----+-----+-----+ 1080
      R L A A G A T L K E L G L T Q D K I K T
CACGGTGCAGCACTGCAGTGCCGCATCACCGGAAGATCCAAACAACGGCTTCCGCCCA
1081 -----+-----+-----+-----+-----+-----+ 1140
      H G A A L Q C R I T T E D P N N G F R P
GATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCTGCTTGACGGT
1141 -----+-----+-----+-----+-----+-----+ 1200
      D T G T I T A Y R S P G G A G V R L D G
GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC
1201 -----+-----+-----+-----+-----+-----+ 1260
      A A Q L G G E I T A H F D S M L V K M T
TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGACAGCGCGCTTGGCTGAGTTC
1261 -----+-----+-----+-----+-----+-----+ 1320
      C R G S D F E T A V A R A Q R A L A E F
ACCGTGTCTGGTGTGCAACCAACATTGGTTTCTTGCGTGCGTTGCTGCGGGAAGAGGAC
1321 -----+-----+-----+-----+-----+-----+ 1380
      T V S G V A T N I G F L R A L L R E E D
TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT
1381 -----+-----+-----+-----+-----+-----+ 1440
      F T S K R I A T G F I G D H P H L L Q A

```

FIG. 1B

1441 CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1500
 -----+-----+-----+-----+-----+-----+
 P P A D D E Q G R I L D Y L A D V T V N
 1501 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC 1560
 -----+-----+-----+-----+-----+-----+
 K P H G V R P K D V A A P I D K L P N I
 1561 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1620
 -----+-----+-----+-----+-----+-----+
 K D L P L P R G S R D R L K Q L G P A A
 1621 TTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1680
 -----+-----+-----+-----+-----+-----+
 F A R D L R E Q D A L A V T D T T F R D
 1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1740
 -----+-----+-----+-----+-----+-----+
 A H Q S L L A T R V R S F A L K P A A E
 1741 GCCGTGCGAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGCGACCTAC 1800
 -----+-----+-----+-----+-----+-----+
 A V A K L T P E L L S V E A W G G A T Y
 1801 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
 -----+-----+-----+-----+-----+-----+
 D V A M R F L F E D P W D R L D E L R E
 1861 GCGATGCCGAATGTAAACATTTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATACACC 1920
 -----+-----+-----+-----+-----+-----+
 A M P N V N I Q M L L R G R N T V G Y T
 1921 CCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGAC 1980
 -----+-----+-----+-----+-----+-----+
 P Y P D S V C R A F V K E A A S S G V D
 1981 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCA 2040
 -----+-----+-----+-----+-----+-----+
 I F R I F D A L N D V S Q M R P A I D A
 2041 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2100
 -----+-----+-----+-----+-----+-----+
 V L E T N T A V A E V A M A Y S G D L S
 2101 GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC 2160
 -----+-----+-----+-----+-----+-----+
 D P N E K L Y T L D Y Y L K M A E E I V
 2161 AAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG 2220
 -----+-----+-----+-----+-----+-----+
 K S G A H I L A I K D M A G L L R P A A

FIG. 1C

2221 GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTTCGATCTGCCAGTGCACGTGCACACC 2280
 -----+-----+-----+-----+-----+-----+
 V T K L V T A L R R E F D L P V H V H T
 2281 CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT 2340
 -----+-----+-----+-----+-----+-----+
 H D T A G G Q L A T Y F A A A Q A G A D
 2341 GCTGTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC 2400
 -----+-----+-----+-----+-----+-----+
 A V D G A S A P L S G T T S Q P S L S A
 2401 ATTGTTGCTGCATTTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT 2460
 -----+-----+-----+-----+-----+-----+
 I V A A F A H T R R D T G L S L E A V S
 2461 GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC 2520
 -----+-----+-----+-----+-----+-----+
 D L E P Y W E A V R G L Y L P F E S G T
 2521 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG 2580
 -----+-----+-----+-----+-----+-----+
 P G P T G R V Y R H E I P G G Q L S N L
 2581 CGTGCACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACCTAC 2640
 -----+-----+-----+-----+-----+-----+
 R A Q A T A L G L A D R F E L I E D N Y
 2641 GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT 2700
 -----+-----+-----+-----+-----+-----+
 A A V N E M L G R P T K V T P S S K V V
 2701 GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC 2760
 -----+-----+-----+-----+-----+-----+
 G D L A L H L V G A G V D P A D F A A D
 2761 CCACAAAAGTACGACATCCCAGACTCTGTTCATCGCGTTCCTGCGCGGCGAGCTTGGTAAC 2820
 -----+-----+-----+-----+-----+-----+
 P Q K Y D I P D S V I A F L R G E L G N
 2821 CCTCCAGGTGGCTGGCCAGAACCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC 2880
 -----+-----+-----+-----+-----+-----+
 P P G G W P E P L R T R A L E G R S E G
 2881 AAGGCACCTCTGACGGAAGTTCCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC 2940
 -----+-----+-----+-----+-----+-----+
 K A P L T E V P E E E Q A H L D A D D S

FIG. 1D

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2941 AAGGAACGTCGCAACAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC
-----+-----+-----+-----+-----+-----+ 3000
      K E R R N S L N R L L F P K P T E E F L
3001 GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA
-----+-----+-----+-----+-----+-----+ 3060
      E H R R R F G N T S A L D D R E F F Y G
3061 CTGGTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTT
-----+-----+-----+-----+-----+-----+ 3120
      L V E G R E T L I R L P D V R T P L L V
3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC
-----+-----+-----+-----+-----+-----+ 3180
      R L D A I S E P D D K G M R N V V A N V
3181 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACC
-----+-----+-----+-----+-----+-----+ 3240
      N G Q I R P M R V R D R S V E S V T A T
3241 GCAGAAAAGGCAGATTCTCCAACAAGGGCCATGTTGCTGCACCATTGCTGGTGTGTC
-----+-----+-----+-----+-----+-----+ 3300
      A E K A D S S N K G H V A A P F A G V V
3301 ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG
-----+-----+-----+-----+-----+-----+ 3360
      T V T V A E G D E V K A G D A V A I I E
3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG
-----+-----+-----+-----+-----+-----+ 3420
      A M K M E A T I T A S V D G K I E R V V
3421 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA
-----+-----+-----+-----+-----+-----+ 3474
      V P A A T K V E G G D L I V V V S *

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FIG. 1E

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

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NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

1
MST HTSSTLPAPK KILVANRGEI AVRAFRAALE
MTAITLGGLL LKGIITLV

51
TGAATVAIYP REDRGSFHRS FASEAVRIGT EGSPVKAYLD IDEIIGAANK

101
VKADAIYPGY GFLSENAQLA RECAENGITF IGPTPEVLDL TGDKSRAVTA

151
AKKAGLPVLA ESTPSKNIDE IVKSAEGQTY PIFVKAVAGG GGRGMRFVAS
D S

201
PDELRLKATE ASREAEAAFG DGAVYVERAV INPQHIEVQI LGDHTGEVVH
S R

251
LYERDCSLQR RHQKVVEIAP AQHLDPELRD RICADAVKFC RSIGYQGAGT

301
VEFLVDEKGN HVFIEMNPRI QVEHTVTEEV TEVDLVKAQM RLAAGATLKE

351
LGLTQDKIKT HGAALQCRIT TEDPNNNGFRP DTGTITAYRS PGGAGVRLDG

401
AAQLGGEITA HFDSMLVKMT CRGSDFETAV ARAQRALAEF TVSGVATNIG

451
FLRALLREED FTSKRIATGF IADHPHLLQA PPADDEQGRI LDYLADVTVN
G

501
KPHGVRPKDV AAPIDKLPNI KDLPLPRGSR DRLKQLGPAA FARDLREQDA

551
LAVTDTTFRD AHQSLLATRV RSFALKPAEE AVAKLTPELL SVEAWGGATY

601
DVAMRFLFED PWDRLDELRE AMPNVNIQML LRGRTVGYT PYPDSVCRAF

651
VKEAASSGVD IFRIFDALND VSQMRPAIDA VLETNTAVAE VAMAYSGDLS

701
DPNEKLYTLD YYLKMAEEIV KSGAHILAIA DMAGLLRPAA VTKLVLTALRR

751
EFDLPVHVHT HDTAGGQLAT YFAAAQAGAD AVDGASAPLS GTTSQPSLSA

FIG. 2A

09492-10101

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

ATCC 21253 pyc
NRRL B-11474 pyc

801 850
IVAAFAHTRR DTGLSLEAVS DLEPYWEAVR GLYLPFESGT PGPTGRVYRH

851 900
EIPGGQLSNL RAQATALGLA DRFELIEDNY AAVNEMLGRP TKVTPSSKVV

901 950
GDLALHLVGA GVDPADFAAD PQKYDIPDSV IAFLRGELGN PPGGWPEPLR

951 1000
TRALEGRSEG KAPLTEVPPEE EQAHL DADDS KERRNSLNRL LFPKPTEEFL

1001 1050
EHRRRFGNTS ALDDREFFYG LVEGRET LIR LPDVRTPLL V RLDAISEPDD

1051 1100
KGMRNVVANV NGQIRPMRVR DRSVESVTAT AEKADSSNKG HVAAPFAGVV

1101 1150
TVTVAEGDEV KAGDAVAIIE AMKMEATITA SVDGKIDRVV VPAATKVEGG
E

1151
DLIVVVS

FIG. 2B

GTGACTGCTATCACCCCTTGGCGGTCTCTTGTGTTGAAAGGAATAATTACTCTAGTGTGCGACT
CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGCGGAAATC
GCGGTCCGTGCTTTCCGTGTCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC
CGTGAAGATCGGGGATCATTCCACCGCTCTTTTGTCTCTGAAGCTGTCCGCATTGGTACT
GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA
GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCGTGTCTGAAAATGCCAGCTTGCC
CGCGAGTGCAGCGGAAACCGGCATTACTTTTATTTGGCCCAACCCAGAGGTTCTTGATCTC
ACCGGTGATAAGTCTCGTGCAGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTGGCG
GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC
CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA
CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCCGGC
GACGGTTCGGTATATGTGCAACGTGCTGTGATTAACCCCGAGCACATTGAAGTGCAGATC
CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT
CGTCACCAAAAAGTTGTGCGAAATTGGCGGACGACAGCATTTGGATCCAGAACTGCGTGAT
CGCATTTGTGCGGATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACC
GTGGAATTCTTGGTGCATGAAAAGGGCAACCACGTTTTCATCGAAATGAACCCACGTATC
CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG
CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC
CACGGTGCAGCACTGCAGTGCAGCATCACACGGAAGATCCAAACAACGGCTTCCGCCCCA
GATACCGGAACATACACCGCTACCGCTCACAGGCGGAGCTGGCGTTCTGTTACGGT
GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAATGACC
TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGACAGCGCGCTTGGCTGAGTTC
ACCGTGTCTGGTGTGCAACCAACATTGGTTTCTTGCCTGCGTTGCTGCGGGAAGAGGAC
TTCATTCCAAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT
CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC
AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCCAACATC
AAGGATCTGCCACTGCCACGCGGTTCCTGAGCGCTGACCGCTGAAGCAGCTTGGCCAGCCGCG
TTTGCTCGTGATCTCCGTGAGCAGGACGCAGTGGCAGTTACTGATACCACCTTCCGCGAT
GCACACAGTCTTTGCTTGGCAGCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG
GCCGTGCGAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCTTGGGCGCGCGACCTAC
GATGTGGCGATGCGTTTCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG
GCGATGCCGAATGATAACATTAGATGCTGCTTCGCGGCGCAACACCGTGGGATACACC
CCGTACCCAGACTCCGTCTGCCGCGCTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC
ATCTTCCGCATCTTCGACGCGCTTAACGAAGTCTCCAGATGCGTCCAGCAATCGACGCA
GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATCTGGTGATCTCTCT
GATCCAAATGAAAAGCTCTACACCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC
AAGTCTGGCGCTCACATTTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG
GTAACCAAGCTGGTCAACGCACTGCGCCGTGAATTGATCTGCCAGTGCACGTGCACACC
CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT
GCTGTTGACGGTGCTTCCGCAACCACTGTCTGGCACCACCTCCAGCCATCCCTGTCTGCC
ATTGTTGCTGCATTCGCGCACACCCGTGCGGATACCGGTTTGAGCCTCGAGGCTGTTTCT
GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC
CCAGGCCCAACCGGTGCGCTTACCGCCACGAAATCCAGGCGGACAGTTGTCCAACCTG
CGTGACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACCTAC
GCAGCCGTTAATGAGATGCTGGGACGCCCCAACCAAGGTCAACCCATCCTCCAAGGTGTT
GGCGACCTCGCACTCCACCTGGTTGGTGGCGGTGTAGATCCAGCAGACTTTGCTGCAGAC
CCACAAAAGTACGACATCCAGACTCTGTCATCGCGTTCTTGCGCGGCGAGCTTGGTAAC
CCTCCAGGTGGCTGGCCAGAACCACTGCGCAGCCCGCGCACTGGAAGGCCGCTCCGAAGGC
AAGGCACCTCTGACGGAAGTTCTTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC
AAGGAACGTCGCAACAGCCTCAACCGCTGCTGTTCCCGAAGCCAACCGAAGAGTTCTCTC
GAGCACCGTGCCTGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA
CTGGTTCGAGGGCGCGAGACTTTGATCCGCTGCCAGATGTGCGCACCCCACTGCTTGT
CGCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC
AACGGCCAGATCCGCCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC
GCAGAAAAGGCAGATTCTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTGTC
ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG
GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG
GTTCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCTGCTTTCCTAA

FIG. 3A

FIG. 3B

MTAITLGGLLLKGIITLVSTHTSSTLPFAKKILVANRGEIAVRAFRAALETGAATVAIYP
REDRGSFHRSFASEAVREGTEGSPVKAYLDIDEIIGAACKVKADAIYPGYGFLSENAQLA
RECAENGITFIGPTPEVLDLTGDKSRAVTAACKAGLPVLAESTPSKNEDDIVKSAEGQTY
PIFVKAVAGGGGGRGMRFVSSPDELRLKATEASREAEAAFGDGSVYVERAVINPQHIEVQI
LGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGT
VEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKT
HGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAQQLGGEITAHFDSMLVKMT
CRGSDFFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQA
PPADDEQGRILDYLDVTVNKPVGVRPKDVAAPIDKLPNIKDLPLPRGSRDRKQLGPAA
FARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATY
DVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAVKEAASSGVD
IFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEEIV
KSGAHILAIKDMAGLLRPAAVTKLVTAALRREFDLPVHVHHTHDTAGGQLATYFAAAQAGAD
AVDGASAPLSGTTSPQSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGT
PGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVV
GDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEG
KAPLTEVPEEEQAHLDAADDSKERRNSLNRLFPKPTEEFLEHRRRFGNTSALDDREFFYG
LVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMNRNVVANVNGQIRPMRVRDRSVESVTAT
AEKADSSNKGHVAAPFAGVVTVTVAEAGDEVKAGDAVAII EAMKMEATITASVDGKIERVV
VPAATKVEGGDLIVVVS

FIG. 3B

Effect of various substrate concentrations on pyruvate carboxylase activity from *C. glutamicum* BF100 (○) and ATCC 21253 (●).

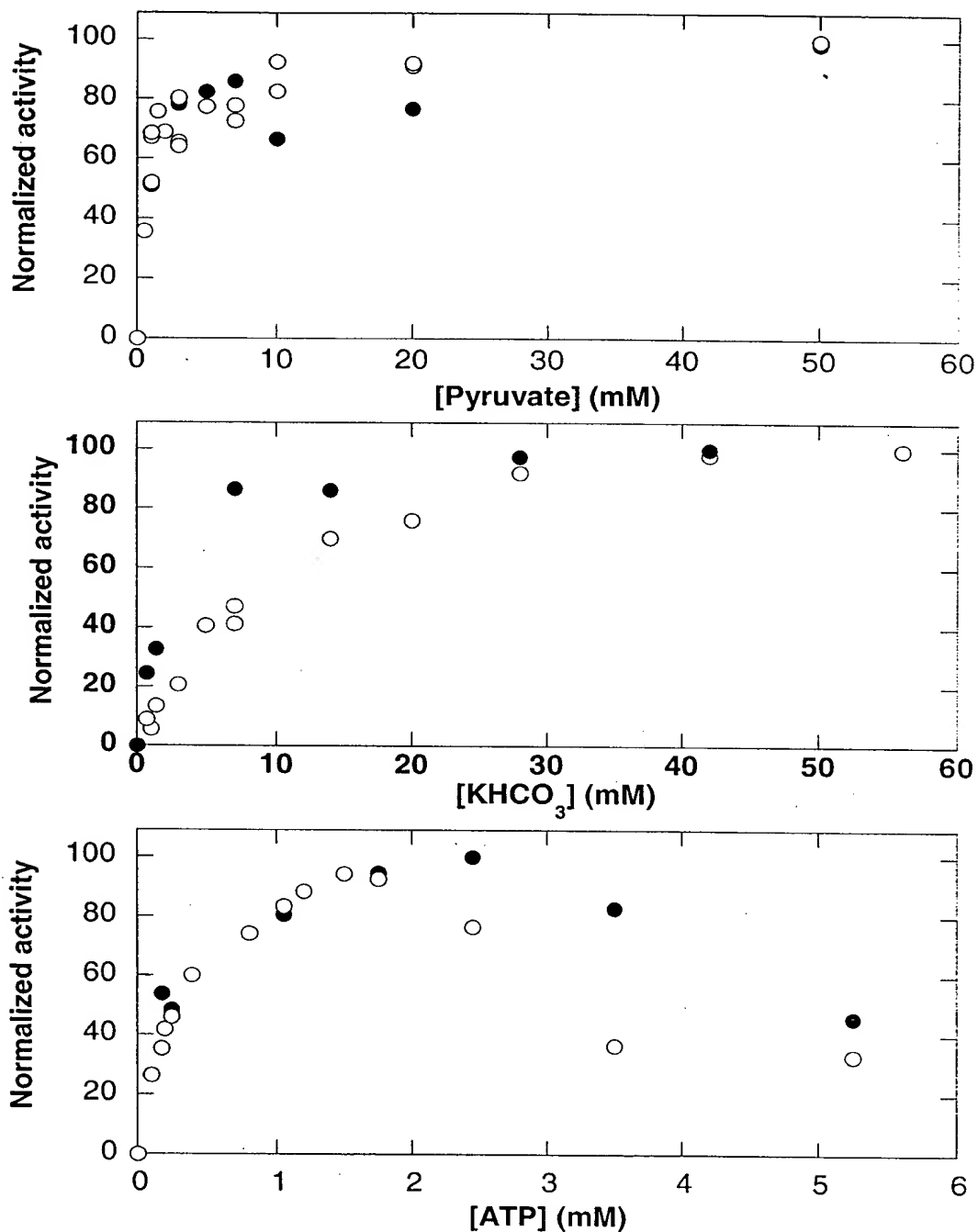


FIG. 4

Effect of aspartate on the activity of pyruvate carboxylase
from *C. glutamicum* BF100 (○) and ATCC 21253 (●).

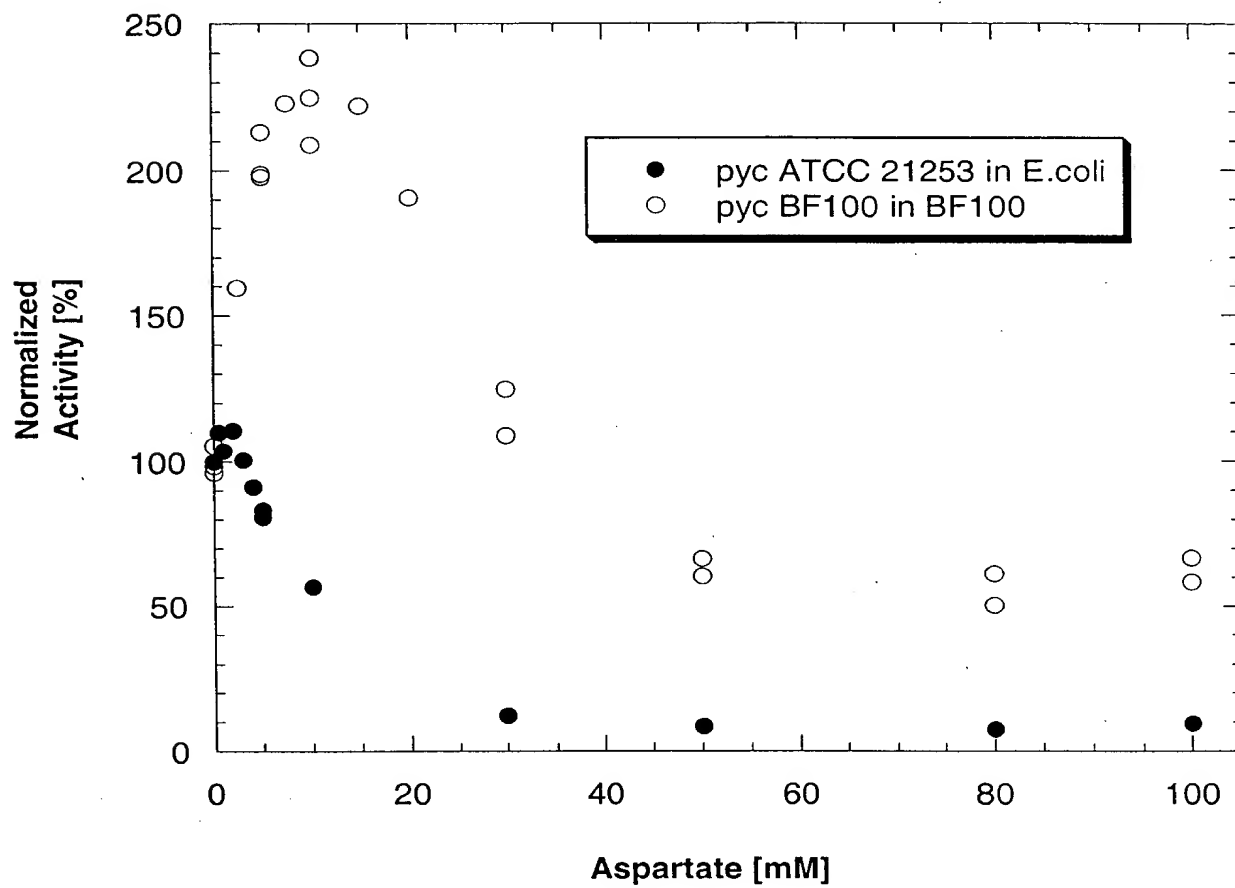


FIG. 5

Effect of Acetyl-CoA on pyruvate carboxylase activity from *C. glutamicum* BF100 (O) and ATCC 21253 (●).

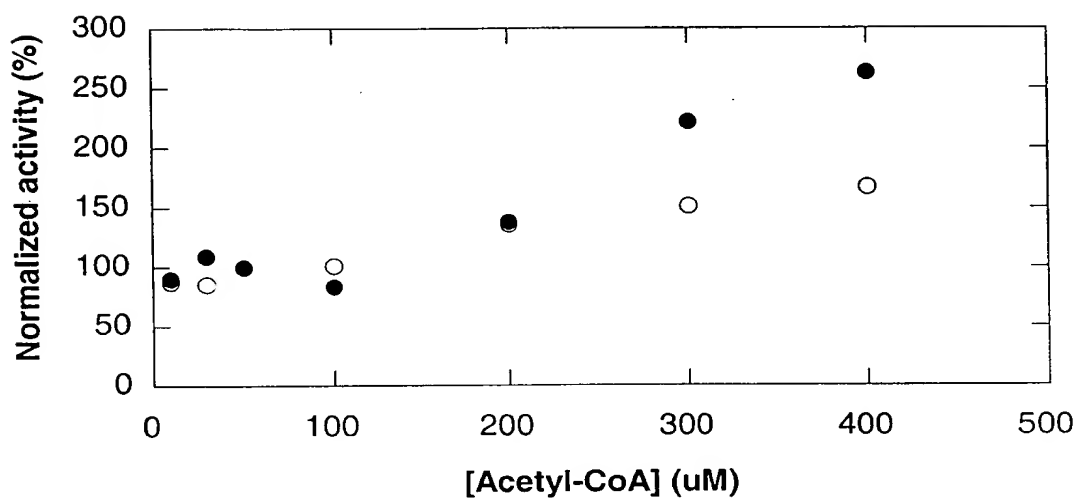


FIG. 6